RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/645,085_

Source: _IPWo_

Date Processed by STIC: _11/17/03_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: **TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: /0/645,085

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFWO

RAW SEQUENCE LISTING   DATE: 11/17/2003
PATENT APPLICATION: US/10/645,085   TIME: 15:15:50

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\11172003\J645085.raw

```
        3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
W-->    4 <120> TITLE OF INVENTION: Agonist antibody
W-->    5 <130> FILE REFERENCE: FP1009
E-->    6 <140> CURRENT APPLICATION NUMBER: US/10/645,085
C-->    6 <141> CURRENT FILING DATE: 2002-10-07
        7 <150> PRIOR APPLICATION NUMBER: JP2000-115246
        8 <151> PRIOR FILING DATE: 2000-04-17
        9 <150> PRIOR APPLICATION NUMBER: JP2000-321821
       10 <151> PRIOR FILING DATE: 2000-10-20
       11 <150> PRIOR APPLICATION NUMBER: JP2000-321822
       12 <151> PRIOR FILING DATE: 2000-10-20
       13 <150> PRIOR APPLICATION NUMBER: PCT/JP01/01912
       14 <151> PRIOR FILING DATE: 2001-03-12
E-->   16 <160> NUMBER OF SEQ ID NOS: 109
```

(handwritten: FYI! all nucleotides MUST be in lower-case letters pp 1-5)

(handwritten circled 109, then 72 (p.5))

ERRORED SEQUENCES

```
     1210 <210> SEQ ID NO: 60
     1211 <211> LENGTH: 115
     1212 <212> TYPE: DNA
     1213 <213> ORGANISM: Artificial Sequence
W--> 1214 <220> FEATURE:
     1215 <223> OTHER INFORMATION: 12B5VH-4
W--> 1216 <400> SEQUENCE: 60
     1217 actcgagacg gtgaccattg tcccttggcc ccagatatcg aaaccataat gtgctcctct   60
E--> 1218 cgcacagtaa tacacagccg tgtcctcggc tctcaggctg ttcatttg                108
     1238 <210> SEQ ID NO: 63
     1239 <211> LENGTH: 433
     1240 <212> TYPE: DNA
     1241 <213> ORGANISM: Human
W--> 1242 <220> FEATURE:
     1243 <221> NAME/KEY: CDS
     1244 <222> LOCATION: (12)...(419)
     1245 <223> OTHER INFORMATION: HEF-12B5H-g gamma. 12-419 peptide
W--> 1246 <400> SEQUENCE: 63
     1247 aagcttccac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga   56
     1248             Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg
     1249              1               5                  10                  15
     1250 ggt gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg 116
     1251 Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
     1252                20                  25                  30                  35
     1253 tcc ctg agt ctc tcc tgt gca gtc tct gga atc acc ctc agg acc tac ggc atg cac tgg 176
```

(handwritten annotations: "108 shown below"; "432 (p.2)"; "Per 1.822 of Sequence Rules, a MAXIMUM of 16 codons per line"; "insert a hard return after 16th codon"; "Met = MET"; "16 codons MAXIMUM per line (please edit)")

/6 Codons per line only

✓ Met

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/645,085

DATE: 11/17/2003
TIME: 15:15:50

Input Set : **A:\PTO.YF.txt**
Output Set: **N:\CRF4\11172003\J645085.raw**

```
1254 Ser Leu Ser Leu Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr Gly (MET) His Trp
1255                  40                  45                  50                  55
1256 gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga 236
1257 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg
1258                  60                  65                  70                  75
1259 agt gaa tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt tcc aag 296
1260 Ser Glu Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys
1261                  80                  85                  90                  95
1262 aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 356
1263 Asn Thr Leu Tyr Leu Gln MET Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
1264                  100                 105                 110                 115
1265 gcg aga gga gca cat tat ggt ttc gat atc tgg ggc caa ggg aca atg gtc acc gtc tcg 416
1266 Ala Arg Gly Ala His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr (MET) Val Thr Val Ser
1267                  120                 125                 130                 135
E--> 1268 agt ggtgagtgga tcc (433) 432
E--> 1269 Ser
     1271 <210> SEQ ID NO: 64
     1272 <211> LENGTH: (323) 321
     1273 <212> TYPE: DNA
     1274 <213> ORGANISM: Human
W--> 1275 <220> FEATURE:
     1276 <221> NAME/KEY: CDS
     1277 <222> LOCATION: (1)...(323)
     1278 <223> OTHER INFORMATION: 12B5LV. 1-323 peptide
W--> 1279 <400> SEQUENCE: 64
```

/6 Codons per line

```
     1280 gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct att gga gac aga gtc acc 60
     1281 Asp Ile Gln (MET) Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr
     1282                  5                  10                  15                  20
     1283 atc acc tgc cgg gcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag aag cca 120
     1284 Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro
     1285                  25                  30                  35                  40
     1286 ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt tta gcc agt ggg gcc cca tca 180
     1287 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser
     1288                  45                  50                  55                  60
     1289 agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240
     1290 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
     1291                  65                  70                  75                  80
     1292 gat gat ttt gca act tat tac tgc caa caa tat agt aat tat ccg ctc act ttc ggc gga 300
     1293 Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly
     1294                  85                  90                  95                  100
E--> 1295 ggg acc aag ctg gag atc aaa (323) 321
     1296 Gly Thr Lys Leu Glu Ile Lys
E--> 1297                  105
     1344 <210> SEQ ID NO: 69
     1345 <211> LENGTH: (110) 102 (p.3)
     1346 <212> TYPE: DNA
     1347 <213> ORGANISM: Artificial Sequence
W--> 1348 <220> FEATURE:
     1349 <223> OTHER INFORMATION: 12B5VL-4
```

```
     RAW SEQUENCE LISTING              DATE: 11/17/2003
     PATENT APPLICATION:  US/10/645,085     TIME: 15:15:50

     Input Set : A:\PTO.YF.txt
     Output Set: N:\CRF4\11172003\J645085.raw

W--> 1350 <400> SEQUENCE: 69
     1351 accatcagca gcctgcagcc tgatgatttt gcaacttatt actgccaaca atatagtaat   60
E--> 1352 tatccgctca ctttcggcgg agggaccaag ctggagatca aa                      102
```

Edit all sequences in which

More than 16 codons per line
are shown

see pp 4-5 for more errors

```
<400> 6
atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca  45
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala
              5                  10                  15
ggt gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg  90
Gly Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu
              10 20              25                  30
gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135
Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
                  35                  40                  45
```

<210> 72 *last sequence in submitted file*
<211> 415
<212> DNA
<213> Human
<220>
<221> CDS
<222> (12)...(398)
<223> HEF-12B5H-g kappa. 12-398 peptide
<400> 72
aagcttccac c atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc 56
           (MET) Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu
            1   5   10   15

tgg ctc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc ctg tct gca 116
116

(format error)
see item 1 on Error Summary (Sheet)

This error appears throughout Sequence 72

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/17/2003
PATENT APPLICATION: **US/10/645,085**   TIME: 15:15:51

Input Set : **A:\PTO.YF.txt**
Output Set: **N:\CRF4\11172003\J645085.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:55; Line(s) 1148,1151,1154,1157,1160
Seq#:63; Line(s) 1250,1251,1253,1254,1256,1257,1259,1260,1262,1263,1265
Seq#:63; Line(s) 1266
Seq#:64; Line(s) 1280,1283,1286,1289,1292
Seq#:65; Line(s) 1308
Seq#:72; Line(s) 1384,1385,1387,1388,1390,1391,1393,1394,1396,1397

Input Set : **A:\PTO.YF.txt**
Output Set: **N:\CRF4\11172003\J645085.raw**

```
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:282 E: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:24 M:283 W: Missing Blank Line separator, <400> field identifier
L:31 M:283 W: Missing Blank Line separator, <220> field identifier
L:33 M:283 W: Missing Blank Line separator, <400> field identifier
L:40 M:283 W: Missing Blank Line separator, <220> field identifier
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:58 M:283 W: Missing Blank Line separator, <220> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:95 M:283 W: Missing Blank Line separator, <220> field identifier
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:134 M:283 W: Missing Blank Line separator, <220> field identifier
L:138 M:283 W: Missing Blank Line separator, <400> field identifier
L:171 M:283 W: Missing Blank Line separator, <220> field identifier
L:175 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:283 W: Missing Blank Line separator, <220> field identifier
L:212 M:283 W: Missing Blank Line separator, <400> field identifier
L:219 M:283 W: Missing Blank Line separator, <220> field identifier
L:221 M:283 W: Missing Blank Line separator, <400> field identifier
L:228 M:283 W: Missing Blank Line separator, <220> field identifier
L:230 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:283 W: Missing Blank Line separator, <220> field identifier
L:239 M:283 W: Missing Blank Line separator, <400> field identifier
L:246 M:283 W: Missing Blank Line separator, <220> field identifier
L:248 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:283 W: Missing Blank Line separator, <220> field identifier
L:257 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:266 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:283 W: Missing Blank Line separator, <220> field identifier
L:275 M:283 W: Missing Blank Line separator, <400> field identifier
L:282 M:283 W: Missing Blank Line separator, <220> field identifier
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:283 W: Missing Blank Line separator, <220> field identifier
L:293 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:283 W: Missing Blank Line separator, <220> field identifier
L:302 M:283 W: Missing Blank Line separator, <400> field identifier
L:311 M:283 W: Missing Blank Line separator, <220> field identifier
L:315 M:283 W: Missing Blank Line separator, <400> field identifier
L:377 M:283 W: Missing Blank Line separator, <220> field identifier
L:379 M:283 W: Missing Blank Line separator, <400> field identifier
L:386 M:283 W: Missing Blank Line separator, <220> field identifier
```

VERIFICATION SUMMARY   DATE: 11/17/2003
PATENT APPLICATION: **US/10/645,085**   TIME: 15:15:51

Input Set : **A:\PTO.YF.txt**
Output Set: **N:\CRF4\11172003\J645085.raw**

L:388 M:283 W: Missing Blank Line separator, <400> field identifier
L:395 M:283 W: Missing Blank Line separator, <220> field identifier
L:399 M:283 W: Missing Blank Line separator, <400> field identifier
L:442 M:112 C: (48) String data converted to lower case,
L:461 M:283 W: Missing Blank Line separator, <220> field identifier
L:465 M:283 W: Missing Blank Line separator, <400> field identifier
L:1218 M:252 E: No. of Seq. differs, <211> LENGTH:Input:115 Found:108 SEQ:60
L:1268 M:254 E: No. of Bases conflict, LENGTH:Input:433 Counted:432 SEQ:63
L:1269 M:252 E: No. of Seq. differs, <211> LENGTH:Input:433 Found:432 SEQ:63
L:1295 M:254 E: No. of Bases conflict, LENGTH:Input:323 Counted:321 SEQ:64
L:1297 M:252 E: No. of Seq. differs, <211> LENGTH:Input:323 Found:321 SEQ:64
L:1311 M:112 C: (48) String data converted to lower case,
L:1352 M:252 E: No. of Seq. differs, <211> LENGTH:Input:110 Found:102 SEQ:69
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (109) Counted (72)